

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/430,590E

DATE: 05/08/2001

TIME: 14:41:23

Input Set : A:\ES.txt

Output Set: N:\CRF3\05082001\I430590E.raw

Does Not Comply
Corrected Diskette Needed

see p 6

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Poulter, et al.
 5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS
 7 <130> FILE REFERENCE: 674521-2001.1
 9 <140> CURRENT APPLICATION NUMBER: 09/430,590E
 10 <141> CURRENT FILING DATE: 1999-10-29
 12 <150> PRIOR APPLICATION NUMBER: 60/106,342
 13 <151> PRIOR FILING DATE: 1998-10-30
 15 <160> NUMBER OF SEQ ID NOS: 156
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 388
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Candida albicans
 24 <300> PUBLICATION INFORMATION:
 25 <308> DATABASE ACCESSION NO: AF043301
 26 <309> DATABASE ENTRY DATE: 1998-07-21
 27 <313> RELEVANT RESIDUES: (1)..(388)
 29 <400> SEQUENCE: 1
 30 tgttcgctat agagagattt cctagccgga atgcacgaca atcctgagac ggaagtcgat 60
 32 cgtcgatgcc catggtgcgt ggtgaaaaat tttcttagaa aatttggtct ttccttcaac 120
 34 tgcttttaag aaagagaggt tcaagtgtt taagtacgac ggtcacaaag attgcggctt 180
 36 atgaggcccg aactgagttg aaatacaaaa tcaagatata attatatacc ttacttgtcc 240
 38 atattgtttt ataatacatt cticagatat ttaaatttct gtgtatcaac ctataaaaca 300
 40 gagatacatt cagtgcattt agtatactga gtgaactggt acctgtgaca ttcaagataa 360
 42 ctgtttcgcg cagcgtggca gacgaaca 388
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 400
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Candida albicans
 50 <300> PUBLICATION INFORMATION:
 51 <308> DATABASE ACCESSION NO: Y08494
 52 <309> DATABASE ENTRY DATE: 1997-08-27
 53 <313> RELEVANT RESIDUES: (1)..(400)
 55 <400> SEQUENCE: 2
 56 cgggttaatg tatatttcga cttgcaggac ctatagaaca gctgtagatg taaacactaa 60
 58 tatgaagaac tgggaaaaca ataacttcta ttctgactct gattctgtat gaaaactaac 120
 60 tgaagaaaag aatataaaaa tataaaatat ataagaagac aaaggagaat ctctgaccct 180
 62 tatatagacc gaaaactaga gtgacgatga accatcagac cagtcaataa ccaactaatt 240
 64 taataatatc aataactcgt ctaacgaggt gtaaacaaaa taccgaaaat agaaatataa 300
 66 ataactcaat gccaaagatgg tgcgcaacca ccaaggtaat aaacaaccaa tagaaccaag 360
 68 aattgtaaat cagacaacga gcaaggctga ttatacaaca 400
 71 <210> SEQ ID NO: 3
 72 <211> LENGTH: 6426
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Candida albicans
 76 <220> FEATURE:
 77 <221> NAME/KEY: CDS

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78 <222> LOCATION: (398)..(1372)
79 <223> OTHER INFORMATION: ORF1 coding sequence for gag
82 <220> FEATURE:
83 <221> NAME/KEY: CDS
84 <222> LOCATION: (1373)..(6103)
85 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
88 <400> SEQUENCE: 3
89 tgttggtttg tgcactatgt tgtgtcagaa actgatcaat gaaaatgatg gttattatga      60
91 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt      120
93 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt      180
95 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt      240
97 acacgctcaa tctcaggtaa agaaagttaa tattccatca gattagaagt cgatagtgat      300
99 aatcatttcg tcccaaatta gcgttgata aattcagtcg tcagatttgt attattgatt      360
101 gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat      415
102                                     Met Ser Ser Ala Lys Asn
103                                     1           5
105 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct      463
106 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
107          10           15           20
109 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc      511
110 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
111          25           30           35
113 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc      559
114 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
115          40           45           50
117 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc      607
118 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
119 55          60           65           70
121 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag      655
122 Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
123          75           80           85
125 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg      703
126 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
127          90           95          100
129 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag      751
130 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
131          105          110          115
133 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat      799
134 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
135          120          125          130
137 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg      847
138 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
139 135          140          145          150
141 ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt      895
142 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
143          155          160          165
145 cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac      943
146 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
147          170          175          180

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149	act	tca	aac	gtt	gtc	gat	gag	tat	gtc	cgt	agt	ctt	cca	aat	ctc	ata	991
150	Thr	Ser	Asn	Val	Val	Asp	Glu	Tyr	Val	Arg	Ser	Leu	Pro	Asn	Leu	Ile	
151			185					190				195					
153	ggt	caa	gtc	ttg	tac	ttc	aat	cat	gtg	aag	aaa	tca	gag	gct	tta	agt	1039
154	Gly	Gln	Val	Leu	Tyr	Phe	Asn	His	Val	Lys	Lys	Ser	Glu	Ala	Leu	Ser	
155		200					205					210					
157	ttg	ttt	ttg	aat	att	cat	gcc	tca	tac	tac	tca	aag	tgg	att	caa	gct	1087
158	Leu	Phe	Leu	Asn	Ile	His	Ala	Ser	Tyr	Tyr	Ser	Lys	Trp	Ile	Gln	Ala	
159	215					220					225				230		
161	gac	aat	gat	aca	tca	gta	ctc	cca	agt	tgc	tct	acc	ata	gct	gaa	gaa	1135
162	Asp	Asn	Asp	Thr	Ser	Val	Leu	Pro	Ser	Cys	Ser	Thr	Ile	Ala	Glu	Glu	
163				235					240			245					
165	atg	tgt	gat	cat	cct	gat	tat	gct	aga	ttg	gtt	gac	att	cca	agc	aac	1183
166	Met	Cys	Asp	His	Pro	Asp	Tyr	Ala	Arg	Leu	Val	Asp	Ile	Pro	Ser	Asn	
167			250					255				260					
169	aaa	tat	gaa	ctt	aat	ctt	att	gtt	agt	tta	cca	gca	cca	gag	aaa	cca	1231
170	Lys	Tyr	Glu	Leu	Asn	Leu	Ile	Val	Ser	Leu	Pro	Ala	Pro	Glu	Lys	Pro	
171		265					270					275					
173	aaa	gga	aaa	cca	gag	gag	aac	tca	ctg	gaa	caa	tct	caa	aag	aag	aac	1279
174	Lys	Gly	Lys	Pro	Glu	Glu	Asn	Ser	Ser	Glu	Gln	Ser	Gln	Lys	Lys	Asn	
175		280				285					290						
177	ctg	aaa	tca	aga	aag	aga	aat	aag	aaa	cat	cca	aaa	tca	gat	aac	gat	1327
178	Ser	Lys	Ser	Arg	Lys	Arg	Asn	Lys	Lys	His	Pro	Lys	Ser	Asp	Asn	Asp	
179	295				300					305					310		
181	aaa	ggt	gaa	aaa	gaa	aaa	gaa	aaa	gaa	aaa	act	tca	ctg	gaa	tga	aaa	1375
182	Lys	Gly	Glu	Lys	Glu	Lys	Glu	Lys	Glu	Lys	Thr	Ser	Ser	Glu		Lys	
183			315					320							325		
185	aca	ggt	gct	gct	tct	att	aat	tgt	gta	atg	aat	ata	cat	aat	tgc	agc	1423
186	Thr	Gly	Ala	Ala	Ser	Ile	Asn	Cys	Val	Met	Asn	Ile	His	Asn	Cys	Ser	
187			330					335							340		
189	aaa	acc	acg	ttt	cca	gta	gaa	aat	tct	cat	tct	ctt	aat	gct	tct	ttg	1471
190	Lys	Thr	Thr	Phe	Pro	Val	Glu	Asn	Ser	His	Ser	Leu	Asn	Ala	Ser	Leu	
191			345					350				355					
193	aac	gta	atg	aat	ttt	aaa	ggt	tta	agg	ttt	aac	aag	tat	cta	gtg	tat	1519
194	Asn	Val	Met	Asn	Phe	Lys	Gly	Leu	Arg	Phe	Asn	Lys	Tyr	Leu	Val	Tyr	
195		360					365					370					
197	gat	act	ggt	gcc	aca	ata	tct	gtt	gtg	aac	aat	aaa	gat	ata	ttg	ctg	1567
198	Asp	Thr	Gly	Ala	Thr	Ile	Ser	Val	Val	Asn	Asn	Lys	Asp	Ile	Leu	Ser	
199		375				380					385						
201	aat	gtt	aag	gac	gca	aca	att	gaa	gtt	tct	gtt	gct	gat	ggt	gct	aca	1615
202	Asn	Val	Lys	Asp	Ala	Thr	Ile	Glu	Val	Ser	Val	Ala	Asp	Gly	Ala	Thr	
203	390					395					400				405		
205	tta	gaa	gca	gat	tgt	att	ggt	gat	cta	att	atc	aga	gtc	ggt	att	gtc	1663
206	Leu	Glu	Ala	Asp	Cys	Ile	Gly	Asp	Leu	Ile	Ile	Arg	Val	Gly	Ile	Val	
207			410					415				420					
209	tcg	att	acg	tta	gag	aat	aca	ttg	tat	tta	cca	gaa	agt	tcc	ttt	aat	1711
210	Ser	Ile	Thr	Leu	Glu	Asn	Thr	Leu	Tyr	Leu	Pro	Glu	Ser	Ser	Phe	Asn	
211			425					430				435					
213	ctt	gtg	agt	ttg	aaa	caa	att	gaa	gaa	cga	gga	ttt	aat	gtt	ctt	att	1759

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214 Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu Ile
215          440          445          450
217 act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att      1807
218 Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile
219          455          460          465
221 att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc      1855
222 Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe
223 470          475          480          485
225 agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat      1903
226 Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp
227          490          495          500
229 atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat      1951
230 Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn
231          505          510          515
233 gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata      1999
234 Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile
235          520          525          530
237 aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat      2047
238 Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr
239          535          540          545
241 gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat      2095
242 Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn
243 550          555          560          565
245 ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta      2143
246 Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu
247          570          575          580
249 caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa      2191
250 Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln
251          585          590          595
253 aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga      2239
254 Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg
255          600          605          610
257 agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga      2287
258 Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg
259          615          620          625
261 ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg      2335
262 Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp
263 630          635          640          645
265 tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att      2383
266 Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile
267          650          655          660
269 att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag      2431
270 Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys
271          665          670          675
273 atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat      2479
274 Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp
275          680          685          690
277 aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att      2527
278 Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile

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281	tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc	2575		
282	Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala			
283	710 715 720 725			
285	gag gtt gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg	2623		
286	Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val			
287	730 735 740			
289	aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat	2671		
290	Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr			
291	745 750 755			
293	tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa	2719		
294	Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln			
295	760 765 770			
297	acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg	2767		
298	Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg			
299	775 780 785			
301	ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa	2815		
302	Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu			
303	790 795 800 805			
305	aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc	2863		
306	Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile			
307	810 815 820			
309	atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg	2911		
310	Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val			
311	825 830 835			
313	ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt	2959		
314	Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg			
315	840 845 850			
317	ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc	3007		
318	Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser			
319	855 860 865			
321	act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga	3055		
322	Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly			
323	870 875 880 885			
325	agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt	3103		
326	Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser			
327	890 895 900			
329	gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat	3151		
330	Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr			
331	905 910 915			
333	tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac	3199		
334	Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn			
335	920 925 930			
337	gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc	3247		
338	Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro			
339	935 940 945			
341	gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg	3295		
342	Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met			
343	950 955 960 965			

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L:5088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85

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L:8916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139

L:9695 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:9695 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: